

Claim Amendments

Claim 1 (original): A method of nucleic acid sequencing comprising the steps:

- (a) amplifying a nucleic acid sample to produce an amplified DNA product;
- (b) extending a sequencing primer bound to the DNA product in the presence of terminating nucleotide analogs to produce a collection of labeled nucleic acid products;
- (c) detecting a total amount of label present in the collection to produce a measurement; and
- (d) combining a plurality of measurements to determine DNA sequence information about the sample.

Claim 2 (original): A method as described in Claim 1 wherein each measurement of a label corresponds to an amount of terminating nucleotide.

Claim 3 (original): A method as described in Claim 1 wherein the DNA sequence information corresponds to a length of the DNA sequence.

Claim 4 (original): A method as described in Claim 1 wherein the DNA sequence information corresponds to a length of the DNA sequence.

Claim 5 (original): A method as described in Claim 1 wherein the DNA sequence information corresponds to a length of the DNA sequence.

Claim 6 (original): A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for diagnostic testing.

Claim 7 (original): A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for genetic localization or gene discovery.

Claim 8 (original): A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for genetic localization or gene discovery.

Claim 9 (original): A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used in conjunction with a DNA database of genetic polymorphisms.

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Claim 10 (original): A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used in conjunction with a DNA database of genetic polymorphisms.

Claim 11 (original): A system for nucleic acid sequencing comprising:

- (a) a means for amplifying a nucleic acid sample to produce an amplified nucleic acid product;
- (b) a means for extending a sequencing primer bound to the DNA product in the presence of terminating nucleotide analogs to produce a collection of labeled nucleic acid products, said extending means in connection with the amplified product;
- (c) a means for detecting a total amount of label present in the collection to produce a measurement, said detecting means in connection with the collection; and
- (d) a means for combining a plurality of measurements to determine DNA sequence information about the sample, said combining means in connection with the measurement.

Claim 12 (original): A system for nucleic acid sequencing comprising:

- (a) a means for amplifying a nucleic acid sample to produce an amplified nucleic acid product;
- (b) a means for extending a sequencing primer bound to the DNA product in the presence of terminating nucleotide analogs to produce a collection of labeled nucleic acid products, said extending means in connection with the amplified product;
- (c) a means for detecting a total amount of label present in the collection to produce a measurement, said detecting means in connection with the collection; and
- (d) a means for combining a plurality of measurements to determine DNA sequence information about the sample, said combining means in connection with the measurement.

Claims 13-16 (canceled)